

Gencore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 23, 2003, 12:05:44 : Search time 74 Seconds
(without alignments)
4242.654 Million cell updates/sec

Title: US-09-804-014A-8
Perfect score: 2918
Sequence: 1 MERRRGTSGRQDKGKDCPG.....VPELPPIWAPPHLTVTEV 559

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 442118 seqs, 280819700 residues
Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100
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-MADLEN=2000000000 -USER=US09804014@cgn.1.1.80.etrnat.20022003.154150.20917
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 2801.5 | 96.0 | 4372 | 10 | US-09-993-811-1 |
| 3 | 2418 | 82.9 | 1792 | 10 | US-09-974-712-3 |
| 4 | 2320 | 79.5 | 1371 | 10 | US-09-974-712-1 |

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|----|--------|------|------|----|---------------------|---------------------|
| 5 | 2218.5 | 76.0 | 3474 | 10 | US-09-993-811-11 | Sequence 11, Appl |
| 6 | 2210.5 | 75.8 | 1599 | 10 | US-09-993-811-4 | GENERAL INFORMATION |
| 7 | 2210.5 | 75.8 | 3473 | 10 | US-09-993-811-5 | Sequence 5, Appl |
| 8 | 1447.5 | 49.6 | 2867 | 10 | US-09-954-436-1227 | Sequence 1227, Appl |
| 9 | 1447.5 | 49.6 | 2867 | 10 | US-09-954-436-1227 | Sequence 2354, Ap |
| 10 | 735.5 | 25.2 | 2847 | 9 | US-10-024-623-10 | Sequence 10, Appl |
| 11 | 728 | 24.9 | 2064 | 12 | US-10-062-879-3 | Sequence 3, Appl |
| 12 | 728 | 24.9 | 2121 | 12 | US-10-062-879-1 | Sequence 1, Appl |
| 13 | 725.5 | 24.9 | 1917 | 12 | US-10-024-623-12 | Sequence 12, Appl |
| 14 | 651.5 | 22.3 | 1844 | 9 | US-10-016-647-3 | Sequence 3, Appl |
| 15 | 649.5 | 22.3 | 468 | 10 | US-09-993-811-8 | Sequence 8, Appl |
| 16 | 649.5 | 22.3 | 2483 | 12 | US-10-143-002-3 | Sequence 3, Appl |
| 17 | 638 | 21.9 | 522 | 10 | US-09-993-811-7 | Sequence 7, Appl |
| 18 | 611.5 | 21.0 | 2127 | 12 | US-10-143-002-1 | Sequence 1, Appl |
| 19 | 600 | 20.6 | 1278 | 9 | US-10-016-647-1 | Sequence 1, Appl |
| 20 | 585 | 20.0 | 998 | 10 | US-09-864-761-1804 | Sequence 1804, Ap |
| 21 | 585 | 20.0 | 1979 | 10 | US-09-864-761-3784 | Sequence 3784, Ap |
| 22 | 578 | 19.8 | 1340 | 10 | US-09-864-761-20550 | Sequence 20550, A |
| 23 | 564 | 19.3 | 492 | 9 | US-09-989-442-11 | Sequence 11, Appl |
| 24 | 564 | 19.3 | 492 | 10 | US-09-989-442-11 | Sequence 22, Appl |
| 25 | 496 | 17.0 | 706 | 10 | US-09-993-811-3 | Sequence 3, Appl |
| 26 | 478.5 | 16.4 | 1668 | 10 | US-09-993-811-13 | Sequence 13, Appl |
| 27 | 416 | 14.3 | 607 | 10 | US-09-864-761-18555 | Sequence 18555, A |
| 28 | 390.5 | 13.4 | 1148 | 10 | US-09-822-849A-405 | Sequence 405, App |
| 29 | 278.5 | 9.5 | 2028 | 10 | US-09-840-125-1 | Sequence 1, Appl |
| 30 | 276.5 | 9.5 | 380 | 10 | US-09-960-352-331 | Sequence 331, App |
| 31 | 247 | 8.5 | 2821 | 10 | US-09-880-107-3358 | Sequence 3358, Ap |
| 32 | 240 | 8.2 | 3074 | 10 | US-09-813-148-1 | Sequence 1, Appl |
| 33 | 237 | 8.1 | 612 | 10 | US-09-864-761-26304 | Sequence 26304, A |
| 34 | 236.5 | 8.1 | 3287 | 9 | US-10-128-870-19 | Sequence 19, Appl |
| 35 | 235.5 | 8.1 | 1887 | 10 | US-09-825-147-3 | Sequence 178, App |
| 36 | 228.5 | 7.8 | 3111 | 10 | US-09-825-147-3 | Sequence 3, Appl |
| 37 | 228 | 7.8 | 2169 | 9 | US-10-128-870-22 | Sequence 22, Appl |
| 38 | 226 | 7.7 | 900 | 9 | US-10-128-870-3 | Sequence 3, Appl |
| 39 | 222 | 7.6 | 2772 | 10 | US-09-825-147-1 | Sequence 1, Appl |
| 40 | 220.5 | 7.6 | 900 | 9 | US-10-128-870-5 | Sequence 5, Appl |
| 41 | 216 | 7.4 | 735 | 9 | US-10-128-870-7 | Sequence 7, Appl |
| 42 | 215 | 7.4 | 2565 | 9 | US-10-128-870-26 | Sequence 26, Appl |
| 43 | 210.5 | 7.2 | 2667 | 10 | US-09-810-796-3 | Sequence 3, Appl |
| 44 | 210.5 | 7.2 | 2694 | 10 | US-09-810-796-2 | Sequence 2, Appl |
| 45 | 210.5 | 7.2 | 3071 | 10 | US-09-810-796-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-989-920-16
: Sequence 16, Application US/0989920
: Patent No. US20020172957A1
: GENERAL INFORMATION:
: APPLICANT: Macina, Roberto
: APPLICANT: Racipon, Herve
: APPLICANT: Chen, Sel-yu
: APPLICANT: Sun, Yonqiang
: APPLICANT: Liu, Chenghua
: TITLE OR INVENTION: Compositions and Methods Relating to Lung Specific Genes and :
: FILE REFERENCE: DD-0291
: CURRENT APPLICATION NUMBER: US/09/989,920
: PRIOR FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: 60/252,500
: NUMBER OF SEQ ID NOS: 284
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 16
: LENGTH: 6823
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-989-920-16
ALIGNMENT Scores:
Pred. No.: 3,38e-194 Length: 6823
Score: 2807.50 Matches: 553
Percent Similarity: 96.35% Conservative: 2

Best Local Similarity: 96.01% Mismatches: 3
Query Match: 96.21% Indels: 20
DB: 9 Gaps: 2
US-09-804-014a-8 (1-559) x US-09-989-920-16 (1-6823)

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QY 41 SerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyAlaThrValPro 60
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DB 245 ACACCGGGCTGGGGCGGC- GCGCGCGGGCGCGAGCGCGCGCGCGCGCGCG 303
QY 87 -----ValGlyAlaThrArgArgPheAlaGlyArgArgGlyCysAlaArgHisGlyAl 104
DB 304 GCGCGGCGCTGGGGCGCACAGCTGGCTTCGGGGTCCGGGGGCTCCGCGCGCATGGAGC 363
QY 104 aAlaValProAlaAlaProCysGlyCysGlyArgGlyValLeuAsnValAlaGlyLe 124
DB 364 CCGGGTGGCGCGCG--CCGGCGGGCTGTCGAGCGGCTGGCTCAAGCTGGCGGGCT 421
QY 124 uArgPheGlnThrArgAlaArgThrLeuGlyArgPheProAspThrLeuGlnLysPr 144
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QY 144 aAlaArgArgGlyArgPheTyrAspAspAlaArgGlyLysTyrPhePheAspArgHisAr 164
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QY 164 gProSerPheAspAlaValLeuTyrTyrGlnSerGlyLysArgLeuArgArgProAl 184
DB 542 GCCACACTTCGAGCGCGCTGCTACTACTACAGTCCGGGGGGCGGCGCGCGCG 601
QY 184 aHISValProLeuAspValPheLeuGlnGlyAlaAlaPheTyrGlyLeuGlyAlaAla 204
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DB 662 CCGGGACCGCTGGCGGAGAGACGAGGCTGCCGGTCCCGCGCGCGCGCGCGCG 721
QY 224 gArgAlaPheAlaArgGlnLeuTyrLeuLeuPheGlnPheProGlnSerSerGlnAlaAl 244
DB 722 CCGCGCGCTTCGCGCGCGCGCGCGCTGCTTCGAGTTTCCGAGAGGCTCAGCGCGC 781
QY 244 aArgValLeuAlaValSerValLeuValIleLeuValSerIleValValPheGlySle 264
DB 782 GCGCGTGGCTGGCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 841
QY 264 uGlnThrLeuProAspPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAl 284
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DB 902 AGCGCGCGCG---TTCCCGCGCTCCGCTGATGCTCCAGCAAAATCCGGAATATCCAC 958
QY 304 oArgLeuProPheAsnAspProPhePheValAlaGlnThrLeuGlyLysTrpPheS 324
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QY 464 rGlyAspMetAlaProValThrValGlyLysIleValGlySerLeuGlySerLeuGlyAlaIleAl 484
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DB 1499 GGGCGTGTACTATTCTCCGTGCAGTGGCGCGCATGCTGCTCCAAATTTACGCTACTTAA 1558
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; Sequence 1, Application US/09993811
; Patent No. US20020119476A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Nucleotide Sequences
; FILE REFERENCE: 00248
; CURRENT APPLICATION NUMBER: US/09/993,811
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (357)..(1727)
US-09-993-811-1

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DB: 10
Gaps: 2
US-09-804-014a-8 (1-559) x US-09-993-811-1 (1-4372)

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QY 164 gProSerPheAspAlaValLeuTyrTyrGlnSerGlyArgLeuArgArgProAl 184
DB 542 GCCCAGCTTCGAGCG 601
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DB 602 GCAGGTGGCG 661
QY 204 AlaLeuAlaArgLeuArgGluAspGluGlySerProValProProGluArgProLeu 224
DB 662 CCGTGGACG 721
QY 224 gArgAlaPheAlaArgGlnLeuTyrPheLeuPheGluPheProGlnSerSerGlnAla 244
DB 722 CCGCGCGCTTCG 781
QY 244 aArgValLeuAlaValAlaSerValLeuValIleLeuValSerIleValValPheCys 264
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QY 264 uGluThrLeuProAspPheArgAspAspArgGlyThrGlyLeuAlaAlaAlaAla 284
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QY 304 oArgLeuProPheAsnAspProPhePheValAlaGluThrLeuCysIleCysTrpPhe 324

DB 959 CCGCGTCCCTGCATGACCCGTTCTTCGTGAGACCCGTCGTATTTGTTGTTCTC 1018
QY 324 rPheGluLeuLeuValArgLeuLeuValLysProSerLysAlaIlePhePheLysAsn 344
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QY 344 lMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuGlyThrGlu 364
DB 1079 GATCAACCTCATGATTTTGTGTATCTTCCTCACTTTGTGTGACATGGGACCGAG 1138
QY 364 uAlaArgGlnArgGlyValGlyGlnAlaMetSerLeuAlaIleLeuArgValIle 384
DB 1139 GCGCGGCGAGAGGCGTGGCGCGAGCGAGCATGTCACTGCGCATCTCGAGAGTCAT 1198
QY 384 gLeuValArgValPheArgGlyPhePheLysLeuSerArgHisSerLysGlyLeuGln 404
DB 1199 ATTGTGCTGTCTTCGCGATCTTCAAGCTGTCCCGCACTCAAAAGGCGCTGCAAA 1258
QY 404 uGlyGlnThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPhe 424
DB 1259 GCGCGAGACGCTTCGGCGCTTCATGCTGAGCTGGGCTCTCTCATCTTTCTTCAT 1318
QY 424 eGlyValValLeuPheSerSerAlaValTyrPheAlaGluValAspArgValAsp 444
DB 1319 CGGTGTGCTCTTTCTTCTGAGCGCGCTCACTTTGCGGAGTTGACCGGGGACCTCC 1378
QY 444 sPheThrSerIleProGluSerPheTrpTrpAlaValAlaThrMetThrValGly 464
DB 1379 TTTCACTAGATCCCTAGCTCTTGTGTGGGCGGTAGTACCATGCTCACTGAGT 1438
QY 464 rGlyAspMetAlaProValThrValGlyLysIleValGlySerLeuGlyAlaIle 484
DB 1439 TGGAGACATGACACCGCTCACTGTGGGTGGCAAGATGTGGCTCTGTGTGCAAT 1498
QY 484 aGlyValLeuThrIleSerLeuProValProValIleValSerAsnPheSerTyrPhe 504
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QY 504 rHisArgGlnThrGluGlyGluAlaGlyMetPheSerHisValAspMetLysPro 524
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QY 524 sGlyProLeuGlnGlyLysAlaAsnGlyLysLeuValAspGlyGluValProGlu 544
DB 1619 TGGCCCACTGAGGCGCAAGGCGCAATGGGCGGTGTGTGAGCGGAGGTACTGAC 1678
QY 544 oProProLeuTrpAlaProProArgGluHisLeuValThrGluVal 559
DB 1679 ACCTCCACTGTGGGCGACCCCGAGGAAACACCTGTGTACCGAAGTG 1724

RESULT 3
US-09-974-712-3
; Sequence 3, Application US/09974712
; Patent No. US20020119540A1
; GENERAL INFORMATION:
; APPLICANT: Fridtjof, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Gerhardt, Brenda
; TITLE OF INVENTION: No. US20020119540A1 Human Ion Channel Protein and Polynucleo
; FILE REFERENCE: LEX-0251-USA
; CURRENT APPLICATION NUMBER: US/09/974,712
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,623
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1792
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-974-712-3

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1,12e-166 | Length: | 1792 |
| Score: | 2418.00 | Matches: | 473 |
| Percent Similarity: | 97.93% | Conservative: | 1 |
| Best Local Similarity: | 97.73% | Mismatches: | 5 |
| Query Match: | 82.86% | Indels: | 6 |
| DB: | 10 | Gaps: | 2 |

US-09-804-014a-8 (1-559) x US-09-974-712-3 (1-1792)

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Db 14 GCGGCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 73
OY 96 ArgArgGlyCysAlaArgHisGlyAlaAvalProAlaAlaProCysGlyCysGlu 115
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Db 74 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 131
OY 116 ArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArg 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 CCGCTGCTGCTCACTGAGCTGGCGCGGCTGCTGAGACCGGCGGCGGCGGCGGCGGCGG 191
OY 136 PheProAspThrLeuLeuGlyAspProAlaAargArgGlyArgPheTyrAspAlaArg 155
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 192 TTCGCGGACACTGCTAGGAGACCCAGCGCGCGCGCGGCTTCTACGACGAGCGGCGG 251
OY 156 ArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrGln 175
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Db 252 CCGGAGTATTTCTTCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 311
OY 176 SerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGluGluVal 195
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Db 312 TCGGCGGCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 371
OY 196 AlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaAargLeuArgGluAspGluCysPro 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 372 GCGTCTCTACGGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 431
OY 216 ValProProGluArgProLeuProArgArgAlaPheAlaArgGluLeuThrLeuPhe 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OY 236 GluPheProGluSerSerGlnAlaAlaAargValLeuAlaValSerValLeuValLe 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 GAGTTTCCCGAGAGCTCTCAGGCGGCGGCGGCGGCTGCGGCTGCGTGGTGCGTGC 551
OY 256 LeuValSerLeuValValPheCysLeuGluThrLeuProAspPheArgAspAspArg 275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 CTCGCTCTCCATCGTGGTCTTTCGCTCGAGCGGCTGCCGACTTCCGCGACGCCGAC 611
OY 276 GlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsnGly 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 GCGACGCGGCGCTGCTGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 668
OY 296 SerSerGlnMetProGlyAsnProArgLeuProPheAsnAspProPhePheVal 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 TCCAGGCAAAATCGTGAATCCACCCCGCTGCCCTCAATGACGCCGTTCTTCGATG 728
OY 316 GluThrLeuCysIleCysTrpPheSerPheGluLeuLeuValArgLeuLeuValCysPro 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 GAGAGCGCTGTGATTTGTGTGTTCTTTCGAGCTGCTGTCGCGCTCTCTGCTGTCCA 788
OY 336 SerLeuAlaIlePhePheLeuAsnValMetAsnLeuIleAspPheValAlaIleLeuPro 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 789 ACCAAGGCTATCTTCTTCAGAACTGATGAACCTCATGATTTGTGGCTATCTCTCC 848
OY 356 TyrPheValAlaLeuGlyThrGluLeuAlaAargGlnArgGlyValGlyGlnGlnAlaMet 375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 849 TACTTTGTGGACACTGGGACCGACGCGGCGGCGGCGGAGGGGTGGCCACGACGCGCATG 908
OY 376 SerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLeuSer 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 909 TCATGCGCATCTGAGATGATCCGATTTGCGGTGTCTTCCGCACTTCAAGCTGTCC 968
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OY 396 ArgHisSerLeuGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetArgGluLeu 415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 969 CCGCACTCAAAAGGCGCTGGAATCTTGGGCGGAGCGCTTGGGCGGCGGCGGCGGCGG 1028
OY 416 GlyLeuLeuIlePhePheLeuPheIleGlyValAlaLeuPheSerSerAlaValTyrPhe 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1029 GCGCTTCATCTTTTCTTCCATCGGCTGAGTGCTCTCTTTCCAGCGCGCTCACTT 1088
OY 436 AlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrpAla 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1089 GCCGAAGTTGACCGGGGTGACCTCCATTTCCATGACATCCCTGAGTCTTCTGTTGGGCG 1148
OY 456 ValValThrMetThrThrThrValGlyTyrGlyAspMetAlaProValThrValGlyLeu 475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1149 GTATGTACCATGACTTACATTTGCTATGAGACATGACCCGCTCACTGTGGTGCAAG 1208
OY 476 IleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValProVal 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1209 ATATGTGGGCTCTGTGTGCTCATTTGGGCGGCGTGAATTTCCCTGCGCACTGCGCGTC 1268
OY 496 IleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluGluAlaGlyMet 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1269 ATTGTCTCCAAATTTACGCTACTTTATCACCGGAGACAGAGCGGAGAACAGGCTGGAGTG 1328
OY 516 PheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyGlyLeu 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1329 TTCAGCATGTGACATGTGACGCTTGTGGCCCACTGGAAGGCAAGCCATGGGGGCTG 1388
OY 536 ValAspGlyGluValProGluLeuProProProLeuTyrPalaProProArgGluHisLeu 555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1389 GTGAGCGGGAGAGTACTGAGTACACCTCCACTGTGGGACACCCCGAAGAACACCTG 1448
OY 556 ValThrGluVal 559
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1449 GTACACGGAAGTG 1460

RESULT 4
US-09-974-712-1
: Sequence 1, Application US/09974712
: Patent No. US20020119540A1
: GENERAL INFORMATION:
: APPLICANT: Fiddle, Carl Johan
: APPLICANT: Hilpun, Erin
: APPLICANT: Gerhard, Brenda
: APPLICANT: Turner, C. Alexander Jr
: TITLE OF INVENTION: No. US20020119540A1el Human Ion Channel protein and Polynucleo
: FILE REFERENCE: LEX-0251-USA
: CURRENT APPLICATION NUMBER: US/09/974,712
: PRIOR APPLICATION NUMBER: 2001-10-10
: PRIOR FILING DATE: US 60/239,623
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1371
: TYPE: DNA
: ORGANISM: homo sapiens
US-09-974-712-1

Alignment Scores:
Pred. No.: 1,02e-159 Length: 1371
Score: 2320.00 Matches: 452
Percent Similarity: 99.12% Conservative: 1
Best Local Similarity: 98.91% Mismatches: 3
Query Match: 79.51% Indels: 2
DB: 10 Gaps: 1

US-09-804-014a-8 (1-559) x US-09-974-712-1 (1-1371)
OY 103 GlyAlaAlaValAlaProAlaAlaProCysGlyCysGluArgLeuValLeuAsnValAla 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 GAGGCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
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QY 123 GlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPheProAspThrLeuGly 142
Db 61 GGGGTGGCTTCGAGAGCGGGCGCGACGCTGGGGCGCTCCGGACACTCTCAGG 120
QY 143 AspProAlaArgArgGlyArgPheTyrAspAspAlaArgArgGlyArgPheAspArg 162
Db 121 GACCGACGGCGCGCGCGCTTCTACGACGACGCGCGCGCGGATTTCTTGACCGG 180
QY 163 HisArgProSerPheAspAlaValLeuTyrTyrTyrGlnSerGlyArgLeuArgArg 182
Db 181 CACCGGCCAGCTTCGAGCGCGCTCTACTACTACAGTCCGTGGGGCGCTCGGGGG 240
QY 183 ProAlaHisValProLeuAspValPheLeuGluValAlaPheTyrGlyLeuGlyAla 202
Db 241 CCGCGCGACGTGGCGCTTCGAGCTCTCTGAAAGAGGTGGCGCTTACGGGCTGGCGG 300
QY 203 AlaAlaLeuAlaArgLeuAArgGluAspGluGlyCysProValProProGluArgProLeu 222
Db 301 GCGGCGCTGGACGCCCTGGCGCGAGAGAGGCGTCCCGGCGCGCGCGCGCGCGCTG 360
QY 223 ProArgArgAlaPheAlaArgGlnLeuTyrPheLeuPheGluPheProGluSerSerGln 242
Db 361 CCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCAG 420
QY 243 AlaAlaArgValLeuAlaValAlaSerValLeuValIleLeuValSerIleValValPhe 262
Db 421 GCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTC 480
QY 263 CysLeuGluThrLeuProAspPheArgAspAspArgGlyThrGlyLeuAlaAlaAla 282
Db 481 TGGCTGAGAGCGCTGCTGACTTCCGCGAGAGCGCGCGCGCGCGCGCGCTGCTGCA 540
QY 283 AlaAlaAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsn 302
Db 541 GCGCGACCGCGCGCG---TTCGCCGCTCGCGCTGAAATGCTCCAGCAAAATCCTGGAAT 597
QY 303 ProProArgLeuProPheAsnAspProPhePheValValGluThrLeuGlyIleCysTyr 322
Db 598 CCAACCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGG 657
QY 323 PheSerPheGluLeuLeuValArgLeuLeuValCysProSerIleValIlePhePheLys 342
Db 658 TTCTCCTTGAGCGCTGAGAGCGCTCTGCTGCTCAAGCAAGGCTATCTTTCAG 717
QY 343 AsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuGlyThr 362
Db 718 AACGTGATGAACCTCATGATTTGTGCTATCTCTTCTTGTGGCACTGGGCAAC 777
QY 363 GluLeuAlaArgGlnArgGlyValGlyGlnAlaMetSerLeuAlaIleLeuArgVal 382
Db 778 GAGGTGGCGCGCGAGCGAGGGGTGGCGAGCGCATGTACGTGCGCATCTCAGAGTC 837
QY 383 IleArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerIleGlyLeuGln 402
Db 838 ATCCGATGTGGGTGTCTTCCGATCTTCAAGCTGTCCGGGCACTCAAGGGGCTGCA 897
QY 403 IleLeuGlyIleThrLeuArgAlaSerMetArgIleLeuGlyLeuLeuIlePhePheLeu 422
Db 898 ATCTGGGCGCGAGCGCTTCGGCGCTCATGTGAGCTGGGCGCTCCATCTTTTCTC 957
QY 423 PheIleGlyValValLeuPheSerSerAlaValIleThrPheAlaGluValAspArgValAsp 442
Db 958 TTTCATCGGTGTGCTCTTCTTCCAGCGCGCTACTTGTCCGAAGTGAACGGGTGAC 1017
QY 443 SerHisPheThrSerIleProGluSerPheTyrPheAlaValIleThrMetThrVal 462
Db 1018 TCCCATTTCACTAGCATCCGATCTCTTCTGCGGTGGCGGAGTCAACATGACAGT 1077
QY 463 GlyTyrGlyAspMetAlaProValThrValGlyGlyLysIleValGlySerLeuCysAla 482
Db 1078 GCGTATGAGACATGCGACCGCTCATGTGTGGTGGCAAGATAGGGGCTCTGTGTGCC 1137

QY 483 IleAlaGlyValLeuThrIleSerLeuProValIleAlaSerAspPheSerTyr 502
Db 1138 ATTCGGGCGCTGCTGACTATTTCTTCCATGTGCGCGCATGTTGCTCCAAATTCAGCTAC 1197
QY 503 PheTyrHisArgGluThrGluGlyGluIleAlaGlyMetPheSerHisValAspMetGln 522
Db 1198 TTTTATCACCGGAGACAGAGGGCGGAAGAGGCTGGATGTTTCACCATGTGACATGTCAG 1257
QY 523 ProCysGlyProLeuGluGlyLysAlaAsnGlyIleLeuValAspGlyGluValProGlu 542
Db 1258 CCTTGTGGCCCATGAGAGGCGCAATGGGGCGGTGGAGCGGGAGGTACTGAG 1317
QY 543 LeuProProLeuThrPheAlaProProArgGluHisLeuValIleThrGluVal 559
Db 1318 CTACCACTCTCATCTGGGCGACCCCGAGGAAACCTGTGACCGAAGTG 1368
RESULT 5
US-09-933-811-11
; Sequence 11, Application US/09993811
; Patent No. US20020119476A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Nucleotide Sequences
; FILE REFERENCE: 00248
; CURRENT APPLICATION NUMBER: US/09/993,811
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)..(1861)
US-09-933-811-11
Alignment Scores:
Pred. No.: 6,75e-152 Length: 3474
Score: 2218.50 Matches: 454
Percent Similarity: 85.14% Conservative: 10
Best local Similarity: 83.30% Mismatches: 61
Query Match: 76.03% Indels: 21
DB: 10 Gaps: 8
US-09-804-014a-8 (1-559) x US-09-933-811-11 (1-3474)
QY 21 ThrGlyLysAlaGlnSerArgArgGlyValArgArgArgArgGlyArgAla 40
Db 268 ACAAGGAAAGTCAAGATGCAACGA-----AAAGCGCGGCTGGCAGTTCACACA 321
QY 41 SerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValPro 60
Db 322 GGTGTGGGAACGCGAGAGGCGGCCCT-----AGCCCGGGGGGTAAACCGCC 372
QY 61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAla----- 74
Db 373 CCTCCCGCGCGCTTGGCGG-----ACTTTCATGCTATTTTACC CGCGCAC 423
QY 75 ArgThrProAspThrGlyHisArgAlaGlyAlaAlaValAlaGlyAlaThrArgPheAla 94
Db 424 CGGACACCGCATGGGCT-----GGTGGCGGCTGGGGCGCACACGTCCTTACC 474
QY 95 GlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCysCys 114
Db 475 GGTGCGCGCGGCTGTGGCGCGCATGAGCCAGCGTGGCCGCGG---CCCTGGCGTGTGTC 532
QY 115 GluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGly 134
Db 533 GAGCGGTGTGTCAACGTGGCGGTGGCTTCAAGACCGCGCGCGACGCTGGCG 592
QY 135 ArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAla 154

Db 593 CGTTCCCGACACGCTGCTGGGGACCCGGTGGCCGACAGCCGTTCTACGAGCCGCG 652
Qy 155 ArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyr 174
Db 653 CGCCCGCAATTTCTTCGACCGACCGCCGACGCTTCGATGGGCTCTACTACTAC 712
Qy 175 GluSerGlyGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGlu 194
Db 713 CAGTCGGGGCGGGCTGAGACGGCCGCGACGCTGCCCTCGACGCTTCTCTGAGAG 772
Qy 195 ValAlaPheTyrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgLysAspGlyCys 214
Db 773 GTGCTCTTCTACGGGCTGGGG---CGGCGGCTGGCGGGCGCGGAGAGAGAGGCTGC 829
Qy 215 ProValProProGluArgProLeuProArgArgAlaPheAlaArgLysLeuTyrLeu 234
Db 830 GCGGTC---GCCGACGCGCGCTGCC---CCGCCCTTTCGCGCTCAGCTCTGCTGCTC 883
Qy 235 PheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValSerValLeuVal 254
Db 884 TTGCAATTTCTGAGAGCTGCGAGGCTGCGCGCTGCTGCGGCTGCTCCGACTGCTC 943
Qy 255 IleLeuValSerIleValValPheCysLeuGluTyrLeuProAspPheArgAspArg 274
Db 944 ATCTGGTCTCCATCGTGGCTTTTGGCTGAGACACTGCGACACTTCCGCGAGACCC 1003
Qy 275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsn 294
Db 1004 GATGACCGCGGGCTCGCGCGGTAGTACTGCTGCTCTCCGCTCGGCTCAAT 1063
Qy 295 GlySerSerGlnMetProGluAsnProArgLeuProArgLeuProPheAsnProPhePheVal 314
Db 1064 GGCTCCAGTCCATGCCAGAGACCCCTCCGACAGCCCTTCAACGATTCATCTTTGTG 1123
Qy 315 ValGluThrLeuCysIleCysTyrPheSerPheGluLeuValAlaArgLeuValCys 334
Db 1124 GTGAGACCTGCTGTATCTGCTGCTGCTCTTGTAGAGTGTGCTGCTGCTGCTGCT 1183
Qy 335 ProSerLysAlaIlePhePheLysAsnValMetAsnLeuIleAspPheValAlaIleLeu 354
Db 1184 CTTAGCAACCTGTCTTCAAGAAATGTGATGAACCTAATGACTTCGTGGCATCTG 1243
Qy 355 ProTyrPheValAlaLeuGlyThrGluLeuValAlaArgGlnArgGlyValGlyGlnAla 374
Db 1244 CTTTACTTCTGCGCCCTGGGACGAGGTTAGCCCGAGGGGTGGGCGACGCGCT 1303
Qy 375 MetSerLeuAlaIleLeuArgValIleArgLeuValAlaArgAlaPheArgIlePheLys 394
Db 1304 ATGTCCCTGGCATCTCAAGGGTCATCCGATGTGCTGCTCTTCCGCACTTCAAGCTC 1363
Qy 395 SerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgLysSerMetArgLys 414
Db 1364 TCCAGGCATTTGAAAGGCTCTACAGATCTTGGTCAGACACTGGGGCTTCATGCGGTGAG 1423
Qy 415 LeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyr 434
Db 1424 CTAGGCTCTCTACTTCTTCTCTTCAATGGGCTGCTCTTCTTTCACAGCGAGCTAC 1483
Qy 435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTyrPTP 454
Db 1484 TTGTGTAAGTGAGACCGGGTGACACCAATTCACAGACATCCCGGAGTCTTTTGTGG 1543
Qy 455 AlaValAlaThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGly 474
Db 1544 GGAGTGGTACCATGACACCGGTTGGCTATGGGACATGGACCCCTGACCGGGGTGGC 1603
Qy 475 LysIleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValPro 494
Db 1604 AAGATGCTGGGCTCTCTGTGTGCAATGGAGTGTGCTACCATCTCTGCTGCTGCGCT 1663
Qy 495 ValIleValSerAsnPheSerTyrPheTyrHisArgGluThrGluGlyGluAlaGly 514
Db 1664 GTCATGCTCTTAACCTTAAGCTTAATTACACCGGGAACAGAGGCGCAAGAGGCGAGG 1723

Qy 515 MetPheSerHisValAspMetGlnProCysGlyProLeuGluGlyLysAlaAsnGlyGly 534
Db 1724 ATGTACAGCCATGTGGACACACAGCCCTGCGTACCTGGAGGGCAAGGCTAATGGGGG 1783
Qy 535 LeuValAspGlyGluValProGluLeuProProLeuTyrProAlaProArgGluHis 554
Db 1784 CTGGTGGACTGCTGAGGCTGGAAGCTCTCCACCACTTGGCCCCCTCGAGGAACAC 1843
Qy 555 LeuValThrGluVal 559
Db 1844 ATGGTGAAGTGGTGC 1858
RESULT 6
US-09-993-811-4
; GENERAL INFORMATION:
; APPLICANT: Pharmacia AB
; TITLE OF INVENTION: Nucleotide Sequences
; FILE REFERENCE: 00248
; CURRENT APPLICATION NUMBER: US/09/993,811
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; JOURNAL: Journal of Biological Chemistry
; VOLUME: 273-
; ISSUE: 10;
; PAGES: 58515857
; DATE: 1998-03-06/
; DATABASE ACCESSION NUMBER: GenBank/AF032099
; DATABASE ENTRY DATE: 1998-04-04
US-09-993-811-4
Alignment Scores:
Pred. No.: 1,03e-151 Length: 1599
Score: 2210.50 Matches: 452
Percent Similarity: 84.77% Conservative: 10
Best Local Similarity: 82.94% Mismatches: 62
Query Match: 75.75% Indels: 21
DB: Gaps: 9
US-09-804-014a-8 (1-559) x US-09-993-811-4 (1-1599)
Qy 21 ThrGlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArgAlaGlyArgAla 40
Db 7 ACAAGGAACCTCAAGATCCACGGA-----AAAGCCGCGGTGGAGTGTTCACA 60
Qy 41 SerArgGlnArgAlaArgGlyArgProValAlaLeuArgProAlaGlyAlaThrValPro 60
Db 61 GGTGTGGGAACGGCAGAGGGCGCCCT-----AGCCCGCGGGGGTTAACACCGCC 111
Qy 61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAla----- 74
Db 112 CCGTCCCGCGGCGCTGGCCG-----ACTTTCATGCTATTTTACCGCGCACAC 162
Qy 75 ArgThrProAspThrGlyHisArgAlaGlyAlaAlaValAlaThrArgArgPheAla 94
Db 163 CGGACACCGGACGCGGT-----GGCTGGCGGTGGGGCCACAGCTCGCTTCACC 213
Qy 95 GlyArgArgGlyCysAlaArgHisGlyAlaAlaValProAlaAlaProCysGlyCys 114
Db 214 GGTGTCCCGGGCTGTGCGGCTGAGGACGACGCTGCGCGCC---CTGCGCTGCTGC 270
Qy 115 GluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGly 134
Db 271 GAGCGCTGTGTCTACAGCTGGCGGGTGGCTTGAACCCGCGCGGACGCTCGC 330
Qy 135 ArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAla 154
Db 331 CCGTCCCGGACACGCTGCTGGGGGACCGCGGCGCGGCGGCTTCAACGAGCGCG 390
Qy 155 ArgArgGluTyrPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyr 174
Db 391 CGGCGGAGTATTCTTTCAGCAGCACCGGCCACGCTTGATGGGTGCTTACTACTAC 450

175 Gloserylglyargleuargargproalalhisvalproleuasnvalpheleuglu 194
195 Valalaphetrglyleuglyalalalaleuualarqleuarggluaspglucys 214
511 GTGCTCTTACAGGGGCGGGG---CGGGGCTGGCGGGCGGCGGAGAGAGAGGCTGC 567
215 ProvalProProgIuarProleuProIargAlarAlphealargluLeuTrpleu 234
568 GCGGTC---GCCGAGCGCGCGCTGCC---CCGCCCTTGGCGCTGAGCTCTGCTGCTC 621
235 PhegluLeuProgluusersergluAlalalalargylleuualavalaserleuVal 254
622 TTGCAATTTCTCGAGCTCGAGGCTGCGCGCTGCTCGCGGCTGCTCGTACTGCTGC 681
255 IleuValSerIleValValPheCysleuGlutThrLeuProAspPheargAspArg 274
682 ATCTGCTCCACATCGTGGCTTTGGCTCGAGACACTGCCAGACTTCCGGAGAGCCG 741
275 AspGlyThrGlyleuAlalalalalalaglyProValPheProAlaProleuAsn 294
742 GATGACCCGGGGCTCGCGCGGTAGCGGTGCTGCTGCTGCTCGCGCCGACTGAAT 801
295 GlySerSerGlnMetProgluAsnProProIargLeuProPheAsnAspProPheVal 314
802 GGGTCCAGTCCCATCGAGGAGGCCCTCCCGAGAGCCCTTCAACGATTCCTTTGG 861
315 ValGluThrLeuCysIleCysTrpPheSerPheGluLeuValAlargLeuValCys 334
862 GTGAGAGCCCTGTATCTCTGCTGCTCTTACGCTGCTGCTGCTGCTGCTGCTGCT 921
335 ProSerIysAlalIephePheIysAsnValMetAsnLeuIleAspPheValAlaIleu 354
922 CCAAGCAAGCTGTCTTCAGAAATGATGAACTAATTGCTTCGCGGCATCTCG 981
355 ProTrpPheValAlaleuGlyThrGluLeuAlarGlnArgGlyValGlyGluAla 374
982 CTTACTTCTGGCGCTCGGGCAGAGATTAAGCCGCGAGCGGGGTGGGCCACCGGCT 1041
375 MetSerLeuAlalIeLeuArgValIleargLeuValAlargValPheargIlePheIysLeu 394
1042 ATGTCCTGGGCATCTTAAGGTCATCCGATTTGGTGGCTCTCCGATCTTCAAGTGC 1101
395 SerArgIleSerIysGlyLeuGlnIleleuGlyIleThrLeuAlargIleSerMetArgGlu 414
1102 TCCAGGCAATTCGAGGGTCTACAGATCTGGGTGAGACACAGCGGGCTTCATCGTGA 1161
415 LeuGlyLeuLeuIlePhePheLeuPheIleGlyValIleuPheSerSerAlaValTyr 434
1162 CTAGGTCTCTCATCTTCTTCTTATTTGGCTGCTCTTCTTCTTCCAGCGAGTCTAC 1221
435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProgluSerPheTrp 454
1222 TTTCCTGAAGTGAAGCGGGTGAACCATTTACACAGCATCCCGAGTCTTTTGGTGG 1281
455 AlAlaValIleThrMetThrValGlyTyrGlyAspMetAlaProValThrValGlyGly 474
1282 GCAATGGTCAACATGACAGCGGTGGCTATGGGAGCATGGACCCGCTGACCGTGGTGGC 1341
475 LysIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValPro 494
1342 AAGATCTGGGCTCTGTGTGGCTTGAAGTGTGCTCAACATCTCTCTGCTGCTGCT 1401
495 ValIleValSerAsnPheSerTrpPheThrHisArgIleuThrGluGlyGluAlaGly 514
1402 GTCATTTGCTCTACTTACTTACTTACACCGGGAGAGAGAGGGGAGAGAGAGAGG 1461
515 MetPheSerHisValAspMetGlnProCysGlyProleuGluGlyValAsnGlyGly 534
1462 ATGTACAGCCATGTGTGACACACAGCCCTGCGTACCTGGAGGGCAAGGCTAATGGGGG 1521

535 LeuValAspGlyGluValProGluLeuProProleuTrpAlaProProArgGluHis 554
1522 CTGGTGAATCTGTGAGTGGCTTGAAGCTCTCCACACTCTGAGCCCTGAGAGGAAACAC 1581
555 LeuValThrGluVal 559
1582 ATGGTGAAGTGAAGTGG 1596

RESULT 7

US-09-993-811-5
Sequence 5, Application US/09993811
Patent No. US20020119476A1
GENERAL INFORMATION:
APPLICANT: Pharmacia AB
TITLE OF INVENTION: Nucleotide Sequences
FILE REFERENCE: 00248
CURRENT APPLICATION NUMBER: US/09/993, 811
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ. ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ. ID NO 5
LENGTH: 3473
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (262)..(1860)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank/NM_010596
DATABASE ENTRY DATE: 2000-01-25
US-09-993-811-5

Alignment Scores:
Pred. No.: 2,56e-151 Length: 3473
Score: 2210.50 Matches: 452
Percent Similarity: 84.77% Conservative: 10
Best Local Similarity: 82.94% Mismatches: 62
Query Match: 75.75% Indels: 21
DB: Gaps: 9

US-09-804-014a-8 (1-559) x US-09-993-811-5 (1-3473)

21 ThrGlyIysAlaGlnSerArgArgGlyValArgArgArgArgGlyAlaGlyAla 40
268 ACAAGAAAGCTCAAGATCCACGGA-----AAAGCGCGGGTGGCAGTGTCCACA 321
41 SerArgGlnAlaArgGlyAlaArgProValAlaLeuArgProAlaGlyValThrValPro 60
322 GGTGTGGAAACGGCAGAGAGCGGCCCT-----AGCCCGCGGGGTAAACACGCCCC 372
61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAla----- 74
373 CCTCCCGCGCGCCTGGCGCG-----ACCTTCATGTCTATTTTACCGCGCGACAC 423
75 ArgThrProAspThrGlnHisArgAlaGlyAlaValAlaGlyAlaThrArgArgPheAla 94
424 CGGACACCCGACGTGGGT-----GCTGCGGGCGCTCGGGCGCACACGCTTCAAC 474
95 GluArgArgGlyCysAlaArgHisGlyAlaAlaValAlaProAlaAlaProCysGlyCysCys 114
475 GGTGCGCGGGCTGTGGCGCGCATGAGGCCAGGGTGGCGCGCGC-----CTGCGCTGCTGC 531
115 GluArgLeuValIleuAsnValAlaGlyLeuArgPheGluThrArgAlaThrValGlyGly 134
532 GAGCGGTGTGTCAACATGGCGGGTGGCTTCAAGACCCCGCGCGACGCTGCGC 591
135 ArgPheProAspThrIleuLeuGlyAspProAlaArgArgGlyAlaArgPheTyrAspAla 154
592 CGCTTCCCGGACAGCTGCTGGGGACCCCGGTGGCGCGACCCCTTCTACAGAGCGGCG 651
155 ArgArgGluTrpPhePheAspArgHisArgProSerPheAspAlaValLeuTyrTyrTyr 174
652 CGCGCCGAGTATTTCTTGACGACGACACCGGCCGCTTCGATGGGAGCTTACTACTAC 711

175 GlnSerGlyArgLeuArgArgProAlaHisValProLeuAspValPheLeuGlnGlu 194
|||||
712 CAGTGGGGGGGGCGGTGAGAGCGCGGCGACAGTCCCTCGACGCTTCTCCGGAGAG 771
195 ValAlaPheThrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuArgGluAspGluGlyCys 214
|||||
772 GTGTCTCTTACAGGGGTGGGG---CGGCGGCTGGCGCGGCTGGGAGGAGCGGCTGC 828
215 ProValProProGluArgProLeuProAlaArgAlaPheAlaArgGlnLeuThrPleLeu 234
|||
829 GGGGTC---GCCGAGGCGCGGCTGGCC---CCGCCCTTGGCGGCTGAGCTGGCTGCCTC 882
235 PheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaValAlaValSerValLeuVal 254
|||||
883 TTGGAACTTCTGAGAGCTGCGAGGCTGGCGGCTGCTGCGGCTGCTCCGACTGCTC 942
255 IleLeuValSerIleValValPheCysLeuGluThrLeuProAspPheArgAspArg 274
943 ATCTGTGCTCCATGCTGTGCTTTTCTCGAGACACTGCGAGACTTCCGCGACGACCG 1002
275 AspGlyThrGlyLeuAlaAlaAlaAlaAlaGlyProValPheProAlaProLeuAsn 294
|||
1003 GATGACCCGGGGGCTCGCGCGGTGAGCGGCTGACTGCTGCTCTCCCTCGCTCAAT 1062
295 GlySerSerGlnMetProGluAsnProProArgLeuProPheAsnAspProPheVal 314
|||||
1063 GGCTCCAGTCCCATGCGGACAGAGCCCTCCCGACAGCCCTTCAACATCATCTTTGAG 1122
315 ValGluThrLeuGlyIleCysTrpPheSerPheGluLeuValArgLeuValCys 334
|||
1123 GTGGAGACCCGTGATGCTGCTGCTCTCTTGGAGCTGCTGCTGCTGCTGCTGCTGCT 1182
335 ProSerIleAlaIlePhePheLysAsnValMetAsnLeuIleAspPheAlaIleLeu 354
|||||
1183 CCTAGCAAGAGCTGTGTTCTTCAAGAAATGATGAACCTAATGACTTGGGCGCAATCCG 1242
355 ProTrpPheValAlaLeuGlyThrGluLeuAlaArgGlyAlaGlyGlnGlnAla 374
1243 CCTTACTTGTGGCCCTGGGCGAGGTTAGCCCGGACGCGGCTGGCCCGCGGCT 1302
375 MetSerLeuAlaIleLeuArgValIleArgLeuValArgValPheArgIlePheLysLeu 394
|||||
1303 ATGTCCCTGGCCATCTTAAAGGATCCATGCTGCTGCTTCCGCAATCTTCAAGCTC 1362
395 SerArgHisSerIleGlyLeuGlnIleLeuGlyGlnThrLeuArgLysSerMetArgGlu 414
|||||
1363 TCCAGGCAATTCGAGGGGTCTACAGATCTGGGTCAAGACACTGGGCTTCCATGCGTGA 1422
415 LeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTrp 434
1423 CTAGGCTCTCATCTTCTTCCCTTCAATGGGCTGCTCTTTCGAGCGAGCTTAC 1482
435 PheAlaGluValAspArgValAspSerHisPheThrSerIleProGluSerPheTrp 454
|||||
1483 TTGCTGAAGTGAACCGGCTGACACCATTTCCACAGCATCCCGGAGTCTTTGTGTG 1542
455 AlaValValThrMetThrThrValGlyTrpGlyAspMetAlaProValThrValGlyGly 1602
1543 GCAGGTGATACCATGACACCGGTTGGCTTATGGGACATGGACCCCTCACCGGTGGC 1602
475 LysIleValGlySerLeuGlyAlaIleAlaGlyValLeuThrIleSerLeuProValPro 1662
1603 AAGATGTGGGCTCTGTGTGTCATTCGAGGTGCTCACCATCTCTGCTGCTGCGCT 1662
495 ValIleValSerAsnPheSerTrpPheTrpHisArgGluThrGluGlyGlnGlyAlaGly 1722
1663 GCATATGCTCTTAACCTTGTACTTTTACACCGGAGACAGAGGCGGAGGAGGAGGAG 1722
515 MetPheSerHisValAspMetGlnProCysGlyProLeuGlnGlyLysAlaAsnGlyGly 1782
1723 ATGTACAGCATGTGGACACACAGCCCTGGGAGACCTGGAGGCGAAGGCTAATGTGGGGG 1782

535 LeuValAspGlyGluValProGluLeuProProLeuTrpAlaProAlaArgGluHis 554
|||||
1783 CTGGTGACTCTGAGGTGCTGATCTTCCACACCACTGCGCCCTGACAGGAACAC 1842
555 LeuValThrGluVal 559
|||
1843 ATGTGACTGAGGTG 1857
RESULT 8
US-09-954-456-1227
; Sequence 1227, Application US/0995456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1227
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1227
Alignment Scores:
Pred. No.: 3,58e-96 Length: 2867
Score: 1447.50 Matches: 338
Percent Similarity: 61.31% Conservative: 63
Best Local Similarity: 51.68% Mismatches: 148
Query Match: 49.61% Indels: 107
DB: 10 Gaps: 20
US-09-804-014A-8 (1-559) x US-09-954-456-1227 (1-2867)
2 GlnArgArgArgThrGlySerArg-----ArgGlnLysAspGlyGluGly 17
|||||
34 GAGAGGCAAGAGACAGGAGCGGCTTCTTGTGACGTAGAGGCCAAGGAGGAGTGGCGCC 93
18 Asp-----ProGlyThrGlyLysAlaGln-----Ser 26
94 CAGCAACCCCAAGCTCTCCACAGAGAGGGCGCGGAGCTGAGACGAGCTGACGCC 153
27 ArgArgGlyArgArgArgArgArgGlyArgAlaGlyArg---AlaSerArgGlnAla 45
|||||
154 AGGCGCCCGCGCGCTGAGTGGGGCGCGGAGCGGCTGACGCTGGCGCGACATGCC 213
46 -----ArgGlyArgProValAlaLeuArgProAla-GlyValThrValProPro 62
|||||
214 CTCTGCTCCCGCCCATGAGATGCGCTGCTGCTGCTGCGAGAACGCGGCTGCTATGACC 273

| | | | |
|----|------|---|------|
| QY | 62 | oSer-----ArpProSerAtpProIaGlyLeuPheTyAlaArgPheProAs | 78 |
| Db | 274 | GTCAAGAGAGGCATGAGGCCCGGGCAGGCTGGGCCACAGGAGAGCTCCAG | 333 |
| QY | 78 | pThrGlyHisArgAlaGlyAlaAlaVal-----GlyAlaThr | 90 |
| Db | 334 | TGTCGCCCGAGCGCTGGGCTTCAGGATGGGCCCAAGAGAGCGGCGCAAGGGGCGCGG | 393 |
| QY | 90 | rArgArgPheAlaGlyArgArgGlyCys----- | 99 |
| Db | 394 | GCAGAGAGAGCAGCGCGAGCTCGGAGTGGCGGCGCTTGCGTCCGCGAGACCGGAGTg | 453 |
| QY | 100 | -----Al | 100 |
| Db | 454 | CGGCGCTTGCCTCCGCTGCCAGAGAGAGCTGCCAGCGCTTGACGGCGCTCCCGAGGAC | 513 |
| QY | 100 | aArgHisGlyAlaAlaValProAla-----Al | 109 |
| Db | 514 | GAGAGAGAAAGAGCGATCCCGGCTGGGACCGGTGAGAGCACAGGCTCTGGGACAGGCG | 573 |
| QY | 109 | aProCysGlyCysCysGluArgLeuValLeuAsnValAlaGlyLeuArgPheGluThrAr | 129 |
| Db | 574 | TCCCTGC---ACCAC-CAGGCGCTCCACATCAACATCTCCGGCTGGCTTGAGAGCGA | 629 |
| QY | 129 | gAlaArgThrLeuLeuLysArgPheProAspThrLeuLeuGlyAspProAlaArgArgGlyAr | 149 |
| Db | 630 | GCTGGGCGCCAGCGCGAGATTTCCCAACACACTCTGGGGGACCCCGCCAAAGCGCTGCC | 689 |
| QY | 149 | gPheTyAspAspAlaArgArgGluTyTrPhePheAspArgHisArgProSerPheAspAl | 169 |
| Db | 690 | GTACTTCGACCCCTGAGGAGAACGATCTTCTTGACCGCAACCGGCCACGCTTCGACGG | 749 |
| QY | 169 | aValLeuTyTrTyTrGlnSerGlyGlyArgLeuArgArgProAlaHisValProLeuAs | 189 |
| Db | 750 | TATCTCTACTACTACCAAGTCGCGGGGCGCGCTCGGAGGCGGATCAACGTCTCCCTCGA | 809 |
| QY | 189 | pValPheLeuGluGluValAlaPheTyTrGlyLeuGlyAlaAlaAlaLeuAlaArgLeuAr | 209 |
| Db | 810 | CGTGTTCGCGGAGAGATACGATCTTCCACAGCTGGGGGAGAGCGAGCGCTTCGCG | 869 |
| QY | 209 | gGluAspGluGlyCysProValProProGluArgProLeuProArgArgAlaPheAlaAr | 229 |
| Db | 870 | CGAGGATGAGGGCTTCATTAAGAAGAGAGAAAGCCCTGCTCGCAGCAGATTTCCAGCG | 929 |
| QY | 229 | gGlnLeuTrPheLeuPheGluPheProGluSerSerGlnAlaAlaArgValLeuAlaVala | 249 |
| Db | 930 | CCAGGTGGGCTTATCTTCGAGTATCCGAGAGAGTCTGGGTCCGGCGGGCGCATTCGCAT | 989 |
| QY | 249 | lValSerValLeuVallIleLeuValSerlIleValValPheCysLeuGluThrLeuProAs | 269 |
| Db | 990 | CGTCTCGGTGTGGTATATCCCATCATCATCATCACTTCTGGTGGAGACACCTCGCTCA | 104 |
| QY | 269 | pPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAlaAlaAlaGlyProValPh | 289 |
| Db | 1050 | GTTCAGGAGATGAAGTGAAGCTGCTCGCGCACCTCGGCGCGCCACACAGCTTCCGCG-- | 1100 |
| QY | 289 | eProAlaPro---LeuAsnGlySerSerGlnMet-----ProGlyAsnPro----- | 303 |
| Db | 1108 | -CCGCGCCCTGGGCGCAAGCGCACCGGGGTGATAGCGCCGCTCTGCGCCTACGAGTGGC | 116 |
| QY | 304 | -ProArgLeuPro-----PheAsnAspProPhePheValValGluThrLeuCysIleCy | 321 |
| Db | 1167 | ACCCTCTCTGCGCCAGGACCTCGGCGCACCTTCTTCATGTGGAGACACGTCGTCAT | 122 |
| QY | 321 | stirPheSerPheGluLeuLeuValArgLeuLeuValCysProSerIlysAlaIlePhePh | 341 |
| Db | 1227 | CTGGTTCACCTTCAGAGCTGCTCGGCCCTTCTTCGCTGCCGCCAGCAAGGACAGGTTCTC | 128 |
| QY | 341 | eLysAsnValMetAsnLeuLeuIleAspPheValAlaIleLeuProTyTrPheValAlaLeuG | 361 |
| Db | 1287 | CCGGAACATCATGAACATCATCATGATGGTGGCATTTCCCTACTTCATTCACCTGGG | 134 |
| QY | 361 | YThrGluLeuAlaArgGlnArg-----GlyValGlyGlnGlnAl | 374 |

| Db | Accession | Gene | Protein | Length | Score |
|---|-----------|---|----------|--------|-------|
| Db | 1347 | CACCGAAGCTGGCAGAGCAGCAGGCGGAGGAGGCGGCCGCAAGATGGGACGACGCG | | 1406 | |
| QY | 374 | ametsrleuAlaIleuArValIleArgIleuValArgValPheArgIlePheIysle | 394 | | |
| Db | 1407 | CATGTCCCTGGCCATCCTCCGAGTCAATCCGCCGTGGCGGGTTCGCCGATCTTCAACT | 1466 | | |
| QY | 394 | userArHisserIysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaIserMetArgI | 414 | | |
| Db | 1467 | CTCCCGGACCTCCAGAGGGGCTGCAGATCTCTGGGCAAGACCTTCGACGGCTCCATGAGGA | 1526 | | |
| QY | 414 | uLeuGlyLeuLeuIlePhePheIleuPheIleGlyValValIleuPheSerIeAlaValTy | 434 | | |
| Db | 1537 | GCTGGGCTGCTCATCTCTCTCTCTTCATCGGGGACATCTCTTCCTCCAGTGGCTGTA | 1586 | | |
| QY | 434 | rPheAlaGlnValAspArgValAlaIspSerHisPheThrSerIleProGluUserPheTrpTr | 454 | | |
| Db | 1587 | CTTCGACAGAGCTGCAGACACCGAGGACCCATTCTCTACATCCCTGACGCTTCTGGTG | 1646 | | |
| QY | 454 | pAlaValValThrMetThrThrValGlyIleGlyIleGlyIleGlyIleGlyIleGlyI | 474 | | |
| Db | 1647 | GGCAGTGTGCATCATGACCCACTGTGGGCTACGCGGACACAGAGCCATCATGCTTGGGGG | 1706 | | |
| QY | 474 | ylsAlaIleValGlySerIleuGlyAlaIleIleIleGlyValIleuThrIleSerIleProValPr | 494 | | |
| Db | 1707 | CACATGTGTGGGCTGCTGTGTGTGCATCGCGGGGCTCCACCATTTGCGCTGCTGTGCTC | 1766 | | |
| QY | 494 | oValIleValIserAsnIspSerIlePheTrpHisArgGlnThrGlyGlyGlyGlyGlyGly | 514 | | |
| Db | 1767 | CGTCATGTGCTCCACACTTCACTACTTCTTACACCGCGGAAAGGATCAGAGAGACCGGC | 1826 | | |
| QY | 514 | ymetPheSerHis-----ValAspMetGlnProCysGly-----Pr | 526 | | |
| Db | 1827 | AGTCTTAAAGGAAGACAGCAGGCGACTCAGACGACGAGG-GCGGGGCTGGACAGAGATGCC | 1885 | | |
| QY | 526 | oleuGlyGlyIleValAlaAsnIleGlyIleuVal-----AspGlyGlyIleVal | 540 | | |
| Db | 1886 | AGCGGAAGGTACGCGGAGCAGGCGGATCTCTGCAAGGCTGGGGGAGACCTCGAGGAATG | 1945 | | |
| QY | 540 | lProGluLeuProProIleuThrPalaProProArgIle | 553 | | |
| Db | 1946 | CAGCACTGCCCGCAAGGCG---CAGCTGCCCGCTAGAGAA | 1982 | | |
| RESULT 9 | | | | | |
| US-09-880-107-2354 | | | | | |
| Sequence 2354, Application US/09880107 | | | | | |
| Patent No. US20020142981A1 | | | | | |
| GENERAL INFORMATION: | | | | | |
| APPLICANT: Horne, Darci T. | | | | | |
| APPLICANT: Vockley, Joseph G. | | | | | |
| APPLICANT: Scherf, Uwe | | | | | |
| TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer | | | | | |
| FILE REFERENCE: 44921-5028-WO | | | | | |
| CURRENT APPLICATION NUMBER: US/09/880,107 | | | | | |
| PRIOR FILING DATE: 2001-06-14 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/211,379 | | | | | |
| PRIOR FILING DATE: 2000-06-14 | | | | | |
| PRIOR APPLICATION NUMBER: US 60/237,054 | | | | | |
| PRIOR FILING DATE: 2000-10-02 | | | | | |
| NUMBER OF SEQ ID NOS: 3950 | | | | | |
| SOFTWARE: Patentin Ver. 2.1 | | | | | |
| SEQ ID NO 2354 | | | | | |
| LENGTH: 2867 | | | | | |
| TYPE: DNA | | | | | |
| ORGANISM: Homo sapiens | | | | | |
| FEATURE: | | | | | |
| OTHER INFORMATION: Genbank Accession No. US20020142981A1 M55513 | | | | | |
| US-09-880-107-2354 | | | | | |
| Alignment Scores: | | | | | |
| Pred. No.: | | 3,58e-96 | Length: | 2867 | |
| Score: | | 1447.50 | Matches: | 338 | |

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|------------------------|--------|---------------|-----|
| Percent Similarity: | 61.31% | Conservative: | 63 |
| Best Local Similarity: | 51.68% | Mismatches: | 148 |
| Query Match: | 49.61% | Indels: | 107 |
| DB: | 10 | Gaps: | 20 |

US-09-804-014A-8 (1-559) x US-09-880-107-2354 (1-2867)

| | | | |
|----|-----|--|-----|
| QY | 2 | GIAATGATGATGTThrglySerArg-----ArgTlnAspArygLyLysGly | 17 |
| Dd | 34 | GAGAGCGAGAGACGAGGGCAGCGGCTTTGACSTCAAGGCCAAAGCAGGGATGCGCC | 93 |
| QY | 18 | Asp-----ProGLyThrGLyLSalagIn-----Ser | 26 |
| Dd | 94 | CAGCAACCCCGAGCTTCCTCCAGAGAGCGCGCCGACGACTGAGCGAGCTGACGC | 153 |
| QY | 27 | ArGaArgGLyArGaTargATarGLyArGLAlaelYarg---AlaserArgInArGLa | 45 |
| Dd | 154 | AGCGCGCGCGGAGCGTAGTAGAGGGGGCGCGGAGCGCGGTGACGTGGGGCGACATGCC | 213 |
| QY | 46 | -----ArgGLyArGrProValAlaLeuArProAla-glyValThrValProProP | 62 |
| Dd | 214 | CTGTGCTCCGCGCCATGAGATGCGCCTGATGCGCTTGAGAGAACGGCGGTGCATGACC | 273 |
| QY | 62 | oSer-----ArgProSerArgProAlaGLyLeuPhenylLaArgThirProAS | 78 |
| Dd | 274 | GTCAGAGAGCGCATGAGCGCGGGAGCTCGGCCACAGGCCAGGGAGAGACTTCAG | 333 |
| QY | 78 | rThrGLyHISArGLaelYALaIaVal-----GLyAlaTh | 90 |
| Dd | 334 | TGTCCCCGAGCGGTGGGTCTGAGGATGGGCCAAAGAGCGCGGCCAAAGGGCGCGGC | 393 |
| QY | 90 | rArgArgPhnealaeLYargArgGLyS----- | 99 |
| Dd | 394 | GCGAGAGAGAGCGCGGACTCGGGAGTCCGGCTTCGCTCCGCTCGCGAGCCGGAGTG | 453 |
| QY | 100 | -----Al | 100 |
| Dd | 454 | CGCGCCCTTGGCTCGCGTCCAGAGAGACTGCACAGCGCTCGACGGCGCGCTCCGAGGAC | 513 |
| QY | 100 | aArgHISGLyALAAlaValProAla-----Al | 109 |
| Dd | 514 | GAGAGAGAGAGAGCGATCCCGCTGGGACGCGTGGAGAGCACAGCTGTGGCACGCGC | 573 |
| QY | 109 | aProCyGLyScySGLyArGLyeuValLeuAsnValAlaGLyleuArphhegiunTrar | 129 |
| Dd | 574 | TTCCTCG---ACCAC-CAGCGCGTCCACATCAACATCTCCGGCTTGCGATTGAGAGCA | 629 |
| QY | 129 | gaLaArgThrLeuGLyArgPherProAsPrHrLeuGLyASPProAlaArgrGLyAr | 149 |
| Dd | 630 | GCTGGGACACCGAGCGAGTTCGCCAACACACATCTCGGGGACCCCGCCAAAGCGCTGCC | 689 |
| QY | 149 | grHeTyArAspaSalArgrArgGLyUTyrPherPhesArGHISArGrProserRheasprAl | 169 |
| Dd | 690 | GTACTGTGACCCCCTGTGAAGAAGAGTCTTCTTGACCGGACCGCGCCAGCTTCGACGG | 749 |
| QY | 169 | aValLeuTyTrTyTrGLInsErGLyArGrLeuArGrProAlahISValProleus | 189 |
| Dd | 750 | TATCCTTACTACTACCAAGTCGGGGCGCCCTCGGAGCGCGGTCAACTTCCTCGGA | 809 |
| QY | 189 | pvalrPhLeuGLUGlValAlaPheryrGLyLeuGLyAlaAlaLeuAlaArgLeuar | 209 |
| Dd | 810 | CGTGTTCGCGAGACAGATACGCTTCACAGCTGGGGGAGCAGAGCGCATGAGCGCTTCGG | 869 |
| QY | 209 | ggLIuAspGLUGLySrProValProProGLyUArGrProLeuProArgrAlaPhelaAr | 229 |
| Dd | 870 | CGAGGATGAGGGCTTCATTAAAGAGAGGAGAAAGCCCTGCTCGCAACAGTTCAGCG | 929 |
| QY | 229 | ggLIeUrTrPhLeuDeurhegiunPherProgiuSerSerGIAlaAlaArgrValLeuAla | 249 |
| Dd | 930 | CGAGGTGTGGCTTATCTTCAGATATCCGAGAGACTCTGGGTCCGCGGGCCATTCGCAT | 999 |
| QY | 249 | IValSerValLeuValILLeuValSerILEValValPhCyLeuGLyUthrLeuProAS | 269 |

| | | | | |
|---|---|------|--|--------|
| D | b | 990 | CGCTCGGCTCTGGTTATCTCTATCTTCATATTCATCATACCTTCCTGCTGGAGACCTTCGCTGA | 1049 |
| Q | y | 269 | pPheATrAspAspArGspelYThrGlyLeuAlaAlaAlaAlaAlaGlyProValPh | 289 |
| D | b | 1050 | GTTCAGGAGATGAACGTGATGGTCCGCCACCTCCGGGGCCCAACAGCTCCCGGCG | - 1107 |
| Q | y | 289 | ePrOAlaPro---LeuAnGlySerSerGlnMet-----ProGlyAsnPro----- | 303 |
| D | b | 1108 | -CCGCGCCCTGGGGCCCAACGGCAGCGGGGTCAAGGCCCGCCCTTGCGCCCTACGCTGC | 1166 |
| Q | y | 304 | -ProArgLeuPro-----PheAnSppProPhePheValAlaGlyIleuPheCysIleCy | 321 |
| D | b | 1167 | ACCGCTCTCTGCCAGGACCTGGCCGACCCCTTCTTCATGCTGGAGACACAGCTGGTAT | 1226 |
| Q | y | 321 | StrPheSerPheGlyIleuLeuValArgLeuLeuValCysProSerLysAlaIlePhePh | 341 |
| D | b | 1227 | CTGGGTACCTTCAGCTGGTCTGCGCTTCTTCGCGCTGCCACAGAGCAGGGTTCTC | 1286 |
| Q | y | 341 | eLysAsnValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaIleuGl | 361 |
| D | b | 1287 | CCGGACATATGATGACATCATCATGTGGTGGCCATCTTCCCTCATCATACCTGGG | 1346 |
| Q | y | 361 | YThrGlyIleuValArgIleuArg-----GlyValGlyGlnGlnAl | 374 |
| D | b | 1347 | CACCGAACTGGCAGACGACGACGCCAGGGGCGAGGAGCGGCCCAAGATGGCAGCAGGC | 1406 |
| Q | y | 374 | aMetSerLeuAlaIleuValArgValIleArgLeuValArgValPheArgIlePheLysLe | 394 |
| D | b | 1407 | CATGTCCCTGGCCATCTCCGAGTCAATCCGCGCTGGTCCGGGTGTTCCGCATCTTCAACT | 1466 |
| Q | y | 394 | uSerArgHisSerLysGlyLeuGlnIleLeuGlyGlnThrLeuArgAlaSerMetAlaGly | 414 |
| D | b | 1467 | CTCCCGGCACCTCAAGGGGCGTGAGATCTGGGCAAGACCTTGCAGGCTCATATGAGGA | 1526 |
| Q | y | 414 | uLeuGlyLeuLeuIlePhePheLeuPheIleGlyValValLeuPheSerSerAlaValTyr | 434 |
| D | b | 1527 | GCTGGGCTGCTATCTTCTTCTCTTCAATCGGGGTCATCCCTCTTCTCAGTGGCGTGA | 1586 |
| Q | y | 434 | rPheAlaGlyValAspArgValAspSerHisPheThrSerIleProGlyuSerPheTyrTr | 454 |
| D | b | 1587 | CTTCGCAGAGGCTGACCAACAGGAGGAAACCATTTCTCTACATCCCTGACGCCCTTGATG | 1646 |
| Q | y | 454 | pAlaValValIleMetThrThrValIleGlyTyrGlyAspMetAlaProValIleThrValGly | 474 |
| D | b | 1647 | GGCAGTGGTACACATGACCACTGGGCTGACGGGCAACAGGAGCCATCACTGTTGGGGG | 1706 |
| Q | y | 474 | YLyAlaIleValAlaSerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValPr | 494 |
| D | b | 1707 | CMAATGTGGGCTCGTGTGTCCATCGCCGGGGTCTCCACCATGGCCCTGCTGTGGC | 1766 |
| Q | y | 494 | oValIleValSerAsnPheSerTyrPheTyrHisArgIleuThrGlyGlyGlnGlyAlaGly | 514 |
| D | b | 1767 | CGTCATGCTCCAACTTCAACTTCTTACACCGGGAAAGGATACAGAGAGCCGGC | 1826 |
| Q | y | 514 | yMetPheSerHis-----ValAspMetGlnProCysGly-----Pr | 526 |
| D | b | 1827 | AGTCTTAAGAAAGACGAGGCACTCAGACAGAGG- GCCGGGCTGGACAGAGAGTCC | 1885 |
| Q | y | 526 | oLeuGlyGlyLyAlaAsnGlyIleuVal-----AspGlyGlyVal | 540 |
| D | b | 1886 | AGCGGAAGGTACGCGGAGCAGGAGGATCTTCTGCAGAGGCTGGGGGACCTGGAGATG | 1945 |
| Q | y | 540 | lProGlyIleuProProLeuThrPalaProProArgIu | 553 |
| D | b | 1946 | CAGCACTGCCCGAAGGCG---CAGCTGGCCCTTAGAGAA | 1982 |


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Db 1592 TGCGTCTCAGGCGTGTAGGTTTGTGAGATCTGAGATTTTCAAGCTCACCCGCA 1651
Qy 397 sserlysglyleuglnlleuglylgnhrleuargalasermetargluendlyle 417
Db 1652 TTTTGTAGGTCTGAGGCTCTGGACATCTCTCGAGTAGACTAATGAATTTTGGCT 1711
Qy 417 uleuilephepheleuPhe1le9lyValleuPheSerSerAlaValTyrPheAla1 437
Db 1712 GCGATAAATTTTCCCTGCGCTAGAGATTGTGATATTGTGTACCATGATCTACATGCCA 1771
Qy 437 uValasparGval-----AspSerHisPheTh 446
Db 1772 G-----AGAGTGGAGCTCAACCTAACGACCCCTTCAGTAGAGACACAGTTCAA 1825
Qy 446 rserileploguserPheTyrTriPalaValTyrMetThrThValGlyTyrGlyAs 466
Db 1826 AAACATTTCCCATTTGGCTTGTGGGCTGTAGTACCATGACTACCTGGGTATGGGA 1885
Qy 466 pMetAlaProValThrValGlyGlyLysIleValGlySerLeuGlyAlaIleAlaGly 486
Db 1886 TATGTACCCCAACATGTGTGAGGATGCTGGTGGGAGCCGTGTGTCTGGCTGGAGT 1945
Qy 486 lleuThrIleSerleuProValProValIleValSerAsnPheSerTyrPheTyr 504
Db 1946 GGTGACAAATAGCCATGCCAGTCTGTCTCATTTGTCAATAATTTTGAATGTACTAC 2000

RESULT 11
US-10-062-879-3
; Sequence 3, Application US/10062879
; Patent No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dikhs, Daniel W.
; APPLICANT: Chang Ling, Hua-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-10-062-879-3

Alignment Scores:
Pred. No.: 3,02e-44 Length: 2064
Score: 728.00 Matches: 186
Percent Similarity: 51.92% Conservative: 85
Best Local Similarity: 35.63% Mismatches: 172
Query Match: 24.95% Indels: 80
DB: 12 Gaps: 15

US-09-804-014a-8 (1-559) x US-10-062-879-3 (1-2064)
Qy 74 AlaArgThrProAspThrGlyHisArgAlaGlyAlaValAlaGlyAlaThrArg-Argph 93
Db 22 GGTGGTGGCTTACAGCTCGCGCGGCTGCGGCCCAAGAGCTGAGTCAACATGGGGGCC 81
Qy 93 eAlaGlyArgArgGlyCys-----AlaArgHisGlyAlaAlaValAlaPr 107
Db 82 GGAAGTGGCGGCTGCTGCTTTGGCCGGGCTGCGGCGCATGGGGATGGCGGGTGGCC 141
Qy 107 cAlaAlaProCys-----GlyCysGlyAlaArgLeuVa 118
Db 142 AACTGCCCATCCCTCCGCGGCCCGCGGCGGACAAAGAACAGCGGACG-GATGAGCTGATTGT 200
Qy 118 lleuAsnValAlaGlyLeuArgPheGlnThrArgAlaArgThrleuGlyArgPheProAs 138

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Db 201 CCTCAACGTGAGTGGGCGGAGGTTCACAGCTGGAGGACACGAGCTGGAGCGCTACCCGGA 260
Qy 138 pThrleuLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArgAluTyr 158
Db 261 CACCTGTCTGGGAGC-ACGAGAAAGAGTTCCTTCAACGAGGACCAAGAGAGTA 317
Qy 158 rPhePheAspArgHisArgProSerPheAspAlaValleuTyrTyrTyrGlnSerGly1 178
Db 318 CTTCCTTCGACCGGAGCCCGAGAGTGTCCGCTGCGCTGCTCAACTTACCCGACG-66 374
Qy 178 ValLeuArgArgProAlaHisValProleuAspValPheleuGlnGluValAlaPheTyr 198
Db 375 GAAGCTGACATACCGCGCTAGAGATCTCTGCTGCTACAGAGACAGAGTGGCTTCTA 434
Qy 198 rGlyleuGlyAlaAlaAlaLeuAla-----ArgLeuAr 209
Db 435 CGGCATCTCCCGAGATCATCGGGACTGCTGCTACGAGAGTACAAAGACCGCAAG 494
Qy 209 gGlu-----AspGlnGlyCysProValProProGluArgProleuPr 223
Db 495 GGAGAACCGCGAGCGGCTATGACGACACACACTCGAGAACCAACAGAGTCCATGCC 554
Qy 223 cArgArgAlaPheAlaArgGlnleuThrleuPheGlnPheProGluSerSerGlnAl 243
Db 555 CTCGCTACACTTCGCCGACACCATGTGGCGGCTTCGAGAACCCCAACACGACGCT 614
Qy 243 aAlaArgValleuAlaValSerValleuValIleleuValSerIleValValPheTy 263
Db 615 GGCCCTGTCTTCTACTACGTAGCTGTCTTCAATGCTGTCTGTGTATCACCACGCT 674
Qy 263 sleuGlnThrleuProAspPheArgAspAspArgGlyThrGlyLeuAlaAlaAla1 283
Db 675 GGTGGAGACGTGCC-TCGGCAG-699
Qy 283 aAlaAlaGlyProValPheProAlaProleuAsnGlySerSerGlnMetProGlyAsnPr 303
Db 700 -----GTCCCGGACCAAGAGTCCGCTGGCGGGA 731
Qy 303 oProArgLeuProPheAsnAspProPhePheValValGlnThrleuGlyIleCysTriPh 323
Db 732 G-----CGCTACTCGTGGCTCTTCTGCTGGACAGCGGCGGTGATATGATCT 782
Qy 323 eSerPheGlnleuLeuValArgleuLeuValGlyProSerIlyAlaIlePhePheLysAs 343
Db 783 CACCGTGGAGTACTCTCTCGGCTCTCGGCTCCACCGCTTACCGTTCATCCGCA 842
Qy 343 nValMetAsnleuIleAspPheValAlaIleleuProTyrPheValAlaLeuGlyThrG1 363
Db 843 CGTCATGACATCATCGACGTGTGGCCATCATGCCCTACTACATC-----GGTCTGGT 896
Qy 363 uleuAlaArgGlnArgGlyValGlyGlnGlnAlaMetSerleuAlaIleleuArgAla1 383
Db 897 CATGACCAACCAAGAGAGCTGTCCGCGCTTCGTGCACAGCTC-----939
Qy 383 eArgLeuValArgValAlaPheArgIlePheLysleuSerArgHisSerIlyGlyleuGln1 403
Db 940 -CGGCTCTCCCGCTTTCAGGATCTTCAAGTTTCCGCCACCTCCAGAGGCTCGGAT 998
Qy 403 eleuGlnThrleuArgAlaSerMetArgGluLeuGlyleuLeuIlePhePheLeuPh 423
Db 999 CCTGGGCTACACACGAGAGCTGTGCCCTCGCAACTCGGCTTCTTCTTCCCTCAC 1058
Qy 423 eIleGlyValleuPheSerSerAlaValTyrPheAlaGluValAspArgValAspSe 443
Db 1059 CATGGCATCATCATCTTGCACATGTGATTTATGCCGAGAGAGGCTCTCTCGGCAG 1118
Qy 443 rHisThrSerIleProGluSerPheTyrTriPalaValAlaValThrMetThrThValG1 463
Db 1119 CAAGTTCACACATCCCTCGCTGTTTGTGACACCATTTGCACCATATGCACACACTGG 1178
Qy 463 yTyrGlyAspMetAlaProValThrValGlyLysIleValGlySerLeuGlyAla1 483

```

Db 1179 ATACGAGACATGGTGGCTTAAGACGATTGTCAGGAGGAGATCTTGCGCTCATCTGCTCTT 1238
QY 483 eAlaGlyValLeuThrIleSerLeuProValIleValIleSerIlePheSerTyrPhe 503
Db 1239 GAGGGGGCTGCTGATTCATGCTCCGCGCAGTCCCTGATGTTTCCAACTTATACCGGAT 1298
QY 503 eTyrHisArg-----GluThrIleGlyIleGlyIleValIleValIlePheSerPhe 518
Db 1299 TTACACACAGAAATCAGACAGCTGATTAAGCAGGAGGACAAAGAGGCGCCCTTGCCAG 1358
QY 518 sValAspMetGlnProCysGlyPro-----LeuGluIleTyrValIleAsnGlyIle 534
Db 1359 GATCCGCTGTCGCAAAACAGACAGCTTGCATGCTACCTGCACAGCAGCAGCGGAGCT 1418
QY 534 yLeuValAspGlyGluValIleProGluLeuProProIleThrAlaProProArgGluIle 554
Db 1419 CCTC-----AAGAGAGCGCTGAGCTG-----ACGGAGCAGCCAGCAAGAGAGACA 1463
QY 554 sLeu 555
Db 1464 CATG 1467

RESULT 12
US-10-062-879-1
: Sequence 1, Application US/10062879
: Patent No. US20020127649A1
: GENERAL INFORMATION:
: APPLICANT: Cockett, Mark I.
: APPLICANT: Dikls, Daniel W.
: APPLICANT: Chang Ling, Hui-Ping
: APPLICANT: Sokol, Patricia T.
: TITLE OF INVENTION: Human Potassium Channel Polypeptides and
: TITLE OF INVENTION: Polypeptides and Uses Therefor
: FILE REFERENCE: ahp-98089
: CURRENT APPLICATION NUMBER: US/10/062,879
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: US/09/178,109
: PRIOR FILING DATE: 1998-10-23
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2121
: TYPE: DNA
: ORGANISM: human
US-10-062-879-1

Alignment Scores:
Pred. No.: 3,12e-44 Length: 2121
Score: 728.00 Matches: 186
Percent Similarity: 51.92% Conservative: 85
Best Local Similarity: 35.63% Mismatches: 172
Query Match: 24.95% Indels: 80
DB: 12 Gaps: 15

US-09-804-014a-8 (1-559) x US-10-062-879-1 (1-2121)

QY 74 AAlaArgThrProAspThrGlyHisArgAlaGlyAlaValAlaGlyAlaThrArg-ArgPhe 93
Db 22 GCTGGTGTGCTAGCGTCCGCGCGGCTGCGGCCCAAGAGCTGAGTGCACCATGCGCGCC 81
QY 93 eAlaGlyValArgGlyCys-----AlaArgHisGlyAlaIleValAlaPhe 107
Db 82 GGAATGGGGCTGCTGCTGCTTTTGGCCCGGCGCTGCGCCATCGGGTGGATGCGCGGCC 141
QY 107 eAlaAlaProCys-----GlyCysCysGluArgLeuVal 118
Db 142 AACTGCCCATGCCCCGCGCGCGCGCGCAAGACAAGCGGCGAG-GATGAGCTGATGT 200
QY 118 lLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPheProAs 138
Db 201 CCTCAAGCTGGTGGCGGAGGTTTCCAGACCTGGAGACCGCGCTGAGCGCTTACCGCGA 260
QY 138 pThrLeuGlyAspProAlaArgArgGlyArgPheTyrAspAspAlaArgArgGlyTyr 158

Db 261 CACCTCTGCTGGCAGC---ACGGAGAGAGATTCTTTTACAGAGAGACACAGAGGCTA 317
QY 158 rPheAspArgHisArgProSerPheAspAlaValLeuTyrTyrTyrGlnSerGlyIle 178
Db 318 CTCTTCGACCGGAGCCCGAGGTGTTCCGCTGCGCTCAACTTATACCGCAG---GG 374
QY 178 yArgLeuArgArgProAlaHisValIleProLeuAspValPheLeuGluIleValAlaPheTyr 198
Db 375 GAACCTGCATACCCGCGCTACAGAGTGCATCTGCTCCTACAGACAGAGCTGGCTTCTA 434
QY 198 rGlyLeuGlyValAlaIleAlaLeuAla-----ArgLeuArg 209
Db 435 CGGCATCTCCCGGAGATCATCGGGAGCTGCTGCTACGAGAGTACAGACCGCAGAG 494
QY 209 gGlu-----AspGluGlyCysProValIleProGluArgProLeuPhe 223
Db 495 GGAGACCGCGAGCGGCTCATGAGCAGACAGACTCGGAGACACAGAGAGAGTCCATGCC 554
QY 223 oArgArgAlaPheAlaArgGlnLeuThrPheLeuPheGluPheProGluSerGlnAl 243
Db 555 CTCGCTGAGCTTCGCGCAGACCATGTCGCGGCTTGGAGAACCCACACACAGACGCT 614
QY 243 aAlaArgValLeuAlaValIleValSerValLeuValIleLeuValSerIleValValPheCys 263
Db 615 GCGCTGCTGCTTCTTACTACGTGACTGCTTCTTATGCTGCTGCTGCTACACCAAGCT 674
QY 263 sLeuGluThrLeuProAspPheArgAspAspArgAspGlyTyrGlyLeuAlaIleAlaAl 283
Db 675 GGTGAGACGGTGCCG-----TGGCGACG----- 699
QY 283 eAlaAlaGlyProValIlePheProAlaProLeuAsnGlySerSerGlnMetProGlyAsnPr 303
Db 700 -----GTCGCGGAGCAGAAAGAGTGCCTGCGGGA 731
QY 303 oProArgLeuProPheAsnAspProPhePheValIleGluThrLeuCysIleCysTrpPhe 323
Db 732 G-----CGTACTCGGTCGCTTCTTCTGCTGACACGCGCTGCTGATGATCTT 782
QY 323 eSerPheGluLeuLeuValAlaArgLeuValCysProSerIleValIlePhePhePhePhe 343
Db 783 CACCGTGGAGTACCTCTCGCGGCTCTTCCGCGGCTCCAGCGCGTACCGCTCATCCGAG 842
QY 343 nValMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAlaLeuGlyThrGln 363
Db 843 CGTCATGAGCATCATCAGCAGTGTGGCATCATCTCCCTACTACATC-----GGTCTGCT 896
QY 363 uLeuAlaArgGlnArgGlyValIleGlyIleAlaMetSerLeuAlaIleLeuArgValIle 383
Db 897 CATGACCAACAGACAGACGTCGCGGCTTGTGTCACGCTC----- 939
QY 383 eArgLeuValArgValPheArgIlePhePheLeuSerArgHisSerIleGlyLeuGlnIle 403
Db 940 -CGGCTCTCCGCTTCAAGATCTCAAGTTCCTCCGCGACATCCAGCGCGCTGCGGAT 998
QY 403 eLeuGlyIleThrLeuArgAlaSerMetArgGluLeuGlyLeuLeuIlePhePheLeuPhe 423
Db 999 CTTGGGCTACACACTGAAGACTGTGCTCCGAACTGGGCTTCTTCTTCTTCTCTCCTAC 1058
QY 423 eIleGlyValAlaLeuPheSerSerAlaValTyrPheAlaGlyAlaValAspArgValAsp 443
Db 1059 CATGGCCATCATCTTGTGCGACTGTGATGTTTATGCGCAAGAGGCTCTCGCGCAG 1118
QY 443 rHisPheThrSerIleProGluSerPheTyrPheAlaValAlaValIleThrMetThrValGln 463
Db 1119 CAAGTTCACAGCATCCCTGCTGTTTGGTATACCATCTGTCCATGACCAACAGCGGG 1178
QY 463 yTyrGlyAspMetAlaProValIleThrValGlyIleGlyIleValIleGlySerLeuCysAlaIle 483
Db 1179 ATACGAGACATGCTGCTTAAGACGATTGACGGAAGATCTTCTGCTCATCTCTCTCT 1238
QY 483 eAlaGlyValLeuThrIleSerLeuProValIleValSerIlePheSerTyrPhe 503


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Db 1179 TTGATATTTGCTACCATGATCTACTATGCGGAG-----AGAGTGGAGCTCAACCTAA 1232
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 442 -----AspSerHisPheThrSerLeuProGluSerPheThrProAla 455
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1233 CGACCCCTTCAGCTAGTACGACACACAGTTCCAAAACATTCCCTGTTGGTCTGGTGGC 1292
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 455 aValValThrMetThrThrValGlyTyrGlyAspMetAlaProValThrValGlyGly 475
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1293 TGTAGTACCATGACTACCTGCTGGTTATGGGATATGTACCCCAACATGTCAGGCAT 1352
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 475 sIleValGlySerLeuCysAlaIleAlaGlyValLeuThrIleSerLeuProValProva 495
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1353 GCTGGTGGAGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGT 1412
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 495 lIleValSerAsnPheSerTyrPheTyr 504
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1413 CATTTGCAATATATTTTGGAAATGACTAC 1440

RESULT 14
US-10-016-647-3
; Sequence 3, Application US/10016647
; Patent No. US20020160475A1
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020160475A1 Human Ion Channel Protein and Polynucleotide
; FILE REFERENCE: LEX-0284-USA
; CURRENT APPLICATION NUMBER: US/10/016,647
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/257,932
; NUMBER OF SEQ. ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-016-647-3

Alignment Scores:
Pred. No.: 9,14e-39 Length: 1844
Score: 651.50 Matches: 187
Percent Similarity: 48.45% Conservative: 78
Best Local Similarity: 34.19% Mismatches: 161
Query Match: 22.33% Indels: 122
DB: 9 Gaps: 21

US-09-804-014A-8 (1-559) x US-10-016-647-3 (1-1844)
Qy 2 GluArgArgArgThrGlySerArgArgGluLysAspGlyLysGlyAspProGlyThr 21
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 271 CAGCGCGGAGATCTGCGAG-----CCAGGCGACC 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 22 ---GlyLysAlaGlnSerArgArgGlyArgArgArgArgGlyArgAla 40
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 CCCGGCCAGCGGAGCGGAGGAGAGCCCGGAGGAGCGCGG----- 345
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 41 SerArgLysAlaArgGlyArgProValAlaLeuArgProAlaGlyValThrValPro 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 346 CCCGAGCGGCGCT----- 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 ProProSerArgProSerArgProAlaGlyLeuPheTyrAlaArgThrProAspThrGly 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 CCCCGTCAGCCAGCGGAGGAGCGAGCC-----CCGCTGGGCGC 399
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 HisArgLysAlaIleAlaValAlaThr---ArgArgPheAlaGlyArgGlyCys 99
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 400 TTGGGGTGGGGGCTGACGCGGGCCCTCGGGCCGAAAGTCCCGCGGGCGGCGAGCCATG 459
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 100 -----AlaArgHisGlyAlaAlaValAlaProAlaAlaProCysGlyCysGlyArgLeu 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 460 ACCTTCGGGCGCAGCGGGGCGCC-----TCGGT 489
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 118 ValLeuAsnValAlaGlyLeuArgPheGluThrArgAlaArgThrLeuGlyArgPhePro 137
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 490 GTGCTGAACGTGGGCGCGCGCGGATTCGCTGTCCGGAGAGCTGCTGAAGACTTCGCC 549
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 138 -----AspThrLeuGlyAspProAlaArgArgPhe----- 150
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 550 CTGGCGCGCGTGAAGCCGCTGCAGAGGCTGCCGCTCCAGAGCGGCGAGCTGAGTGTGC 609
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 151 -----TyrAspAlaArgArgGlyTyrPhePheAspArgHisArgProSerPheAsp 168
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 610 GAGCACTACACCGCGAGCCCAACAGTACTTCTTCACCGGAGCTGGAGGCTTCGGC 669
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 169 AlaValLeuTyrTyrGlnSerGlyArgLeuArgArgProAlaHisValProLeu 188
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 670 TTCACTCTGCTTACGTCGCGCGCGGACGGAAGCTGCTTCGCGCGCGGAGTGTGCAG 729
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 189 AspValPheLeuGlnGluValAlaPheTyrGlyLeuGlyAlaAlaLeu----- 205
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 730 CTCCTCTTCAACAAGAGATGATCTACTGGGCGCTGGAGGCGCGACCTCGAGTATCG 789
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 206 AlaArgLeuArgGluAspGlu-GlyCys-----ProValProGluArgProLeu-- 222
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 790 TGCAGCGCGCGCTCGACGAGCCGATGTCGACACTACCTTCTACTGCTGCTGCTGCTG 849
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 223 -----ProArgArgAlaPheAlaArg 229
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 850 CCGGGCGCTGCTGGGCGCGCGAGAGGCGCGCGCGCGCGCGCGCGCGCTGCC--TCCAG 908
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 229 gGlnLeuTyrPheLeu-----LeuPheGluPheProGluSerArgAlaAla 244
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 909 GCGC---TGGCTGAGGCGCATGCGCGGACCTTGAGAGACCCAGCTGCTGCTGCTGCTG 965
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 244 aArgValLeuAlaValSerValLeuValIleLeuValSerIleValValPheCysLe 264
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 966 GCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1025
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 264 uGluThrLeuProAspPheArgAspAspArgAspGlyThrGlyLeuAlaAlaAlaAla 284
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1026 CAGCAGCTGCTGCCAGCTGGCGCAC-----GCAGC 1055
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 284 aAlaGlyProValPheProAlaProLeuAsnGlySerSerGlnMetProGlyAsnProPr 304
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1056 CGCCGAC-----AACCGAGC----- 1071
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 304 aArgLeuProPheAsnAspProPhePheValAlaGluThrLeuGlyIleCysTrpPheSe 324
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1072 -----CTGATGACCGGAGCAGAGATATGAGATATGATGATGATGATGATGATGAT 1121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 324 rPheGluLeuLeuValArgLeuLeuValCysProSerLysAlaIlePhePheLysAsnVa 344
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1122 TGCGAGTGCATCTGTGAGGTTGATCTCCAAAACAGCTGATGTTGTCAAGAGACC 1181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 344 lMetAsnLeuIleAspPheValAlaIleLeuProTyrPheValAla---LeuGlyTrpG 363
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1182 CTTGAACATCTTATATTACTGCGCAATCAGCCGCTATTTACTCTCTGTGTTGATGACAGT 1241
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 363 uLeuAlaArgGlnArgGlyValGlyGlnAlaMetSerLeuAlaIleLeuArgValI 383
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1242 GTTTACAGCGAGAACTCTCAACTCCAGAGGCTGGA-----GTCACTTGAAGGACT 1295
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 383 eArgLeuValArgValPheArgIlePheLysLeuSerArgHisSerLysGlyLeuGlnI 403
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1296 TAGAATGATGAGATTTTGGTGGATTAAGCTTGGCCGCTCACTTCACTTGTGCTTCAGAC 1355
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 403 eLeuGlyGluThrLeuArgLysMetArgGluLeuGlyLeuLeuPhePheLeuPhe 423
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1356 ACTGCGTTTGACTCTCAACCTTCTTACCGAGAGATGTTATGTTACTTCTTCTTCACTTG 1415
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 423 eIleGlyValValLeuPheSerSerAlaValTyrPheAlaGlu-----ValAs 439
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1416 TGTTCATGAGCATCTTATATGACATTCTTCACCTTTCGAACATGGGCTGAGACTGGA 1475
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```


